159192

From:	Gibbs, Terra
Sent:	Wednesday, July 13, 2005 1:47 PM
To:	Jones, Maude
Subject:	FW: Please compare these two sequences... PLEASE RUSH

RE: USSN 09/918,026

-----Original Message-----

From:	Fredman, Jeffrey
Sent:	Wednesday, July 13, 2005 6:10 AM
To:	STIC-Biotech/ChemLib
Cc:	Gibbs, Terra
Subject:	FW: Please compare these two sequences... PLEASE RUSH

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From:	Gibbs, Terra
Sent:	Tuesday, July 12, 2005 5:29 PM
To:	Fredman, Jeffrey
Subject:	Please compare these two sequences... PLEASE RUSH

Jeff, I need this seqeunce search comparison RUSHED! I need this to support a 103 rejection and didn't realize it til now... This case is due this biweek.
The two sequences are only 1561 and 1981 nucleotides in length.

Please compare GenBank Accession Number AF099031 with AF059203.

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
Mailbox 2C18
571-272-0758

1

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OM nucleic - nucleic search, using sw model

                    GenCore version 5.1.6
              Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:        July 14, 2005, 16:47:20 ; Search time 2 Seconds
                                          (without alignments)
                                  3.201 Million cell updates/sec

Title:         AF099031
Perfect score: 1569
Sequence:      1 ATGGAGCCAGGCGGGGGCCCG.........CTTGGTCCTGCCATACCTAG 1569

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 0.5

Searched:      1 segs, 2040 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1 summaries

Database :     af059203.gb_pr:*

   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.

                          SUMMARIES

Result            Query
No.     Score   Match  Length  DB  ID          Description
-----   -----   -----  ------  --  --------     -----------
  1    1564.2   99.7    2040    1  AF059203     ACCESSION:AF059203

                          ALIGNMENTS

RESULT 1
AF059203
LOCUS       AF059203      2040 bp    mRNA      linear   PRI 15-OCT-1998
DEFINITION  Homo sapiens acyl coenzyme A:cholesterol acyltransferase 2 mRNA,
            complete cds.
ACCESSION   AF059203
VERSION     AF059203.1  GI:3746534
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2040)
  AUTHORS   Oelkers,P., Behari,A., Cromley,D., Billheimer,J.T. and Sturley,S.L.
  TITLE     Characterization of two human genes encoding acyl coenzyme
            A:cholesterol acyltransferase-related enzymes
  JOURNAL   J. Biol. Chem. 273 (41), 26765-26771 (1998)
  MEDLINE   98434592
   PUBMED   9756920
REFERENCE   2 (bases 1 to 2040)
  AUTHORS   Oelkers,P., Cromley,D., Behari,A., Billheimer,J.T. and Sturley,S.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-APR-1998) Human Nutrition, Columbia University, 630
            W. 168th Street, New York, NY 10032, USA
FEATURES             Location/Qualifiers
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                     /chromosome="12"
                     /cell_type="hepatocyte"
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                     VFIIRKSLLDELMEVQHPRTIYHMFIAGLCVPIISTLAIDPIDEGRLLEFDLLIFSF
                     GQLPLAIVTWVPMFLSTLLAPYQALRLWARGTWTQATGLGCALLAAHAVVLCALPVHV
                     AVEHQLPPASRCVLVFEQVRFLMKSYSPLREAVPGTLRARRGEGIQAPSFSSSYLYFLF
                     CPTLIYRETYPRTPYVRWNYVAKNFAQALGCVLYACFLGRLCVPVFANMSREPFSTR
                     ALVLSILHATLPGIFMLLIFPAFLHCWLNAFAEMLRFGDRMFYRDWWNSTSFSNYYR
                     TWNVVHDWLYSVYVQDGLRLLGARARGVAMLGVFLVSAVAHEYIFCFVLGFFYPVML
                     ILFLVIGGMLNFMMHDQRTGPAWNVLWMTMLFLGQGIQVSLYQEEWYARRHCPLPQAT
                     FWGLVTPRSWSCHT"

Query Match            99.7%;  Score 1564.2;  DB 1;  Length 2040;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 1566;  Conservative 0;  Mismatches 0;  Indels 3;  Gaps 0;

Qy     1 ATGGAGCCAGGCGGGGGCCCGTTCTGCGTTCTGCAGGACAGCAGAAGGGCTGGAGGGGAGCGGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    52 ATGGAGCCAGGCGGGGGCCCGTTCTGCGTTCTGCAGGACAGCAGAAGGGCTGGAGGGGAGCGGG 111

Qy    61 GAGCGCCAACCCTGTGGAGATGGAAACACTGAGACGCACAGAGCCCCGGACTTGGTACAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   112 GAGCGCCAACCCTGTGGAGATGGAAACACTGAGACGCACAGAGCCCCGGACTTGGTACAA 171

Qy   121 TGGACCCGACACATGAGGAGGCTGTGAAGGCACAATTGCTGAGCAGGCGCAGGGACAACTG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   172 TGGACCCGACACATGAGGAGGCTGTGAAGGCACAATTGCTGAGCAGGCGCAGGGACAACTG 231

Qy   181 AGGGAGCTGCTGGATCGGGCCATGGGGCCATGGGGAGGCTATACAATCCTACCATCACAGACAAA 240
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Qy   241 CCTCTGCCCCCACCTCCCCCAGGTTCCTTGAGCAGGACCCCAGGAGCCATCCCTGGGGAAA 300
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Qy   301 CAGAAAGTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGGAGTGCAGCATTC 360
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Qy   361 CGCACCATCACCACATGTTCATCGCTGTCGTGTCTTCATCATCAGCACCCTGGCC 420
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Db   412 CGCACCATCACCACATGTTCATCGCTGTCGTGTCTTCATCATCAGCACCCTGGCC 471

Qy   421 ATCGACTTCATTGATGAGGGCAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 480
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Db   472 ATCGACTTCATTGATGAGGGCAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 531

Qy   481 GGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGTCCACCCTGTTGGCG 540
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Db   532 GGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGTCCACCCTGTTGGCG 591

Qy   541 CCGTACCAGGCCCTACGGCTGTGGGCCAGGGGCACCTGGACGGGCGACGGGCCTGGGGC 600
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Qy   601 TGTGCGCTTTAGCGCCGCACGGCGTGGTCTCGCGGCCTCCACGTGGCCGTG 660
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Qy   661 GAGCATCAGCTCCCGCCCGGCCTTCCGGTCCTCGGTCTTCGAGCAGGTTAGGTTCCTG 720
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Db   712 GAGCATCAGCTCCCGCCCGGCCTCCCGGTCCTCGGTCTTCGAGCAGGTTAGGTTCCTG 771
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Qy    721 ATGAAAAGCTACTCCTTCCTGAGAGAGGCTGTGCCTGGGATCCTTCGTGCCAGACGAGGT 780
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Db    772 ATGAAAAGCTACTCCTTCCTGAGAGAGGCTGTGCCTGGGACCCTTCGTGCCAGACGAGGT 831

Qy    781 GAGGGGATCCAGGCCCCCAGTTTCTCCAGCTACCTCCTCTCTCTGCCCAACACTC 840
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Db    832 GAGGGGATCCAGGCCCCCAGTTTCTCCAGCTACCTCCTCTCTCTGCCCAACACTC 891

Qy    841 ATCTACAGGGGAGACTTACCCTAGGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAAC 900
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Qy    901 TTTGCCCAGGCCCTGGGATGTGCTTCATGCCTGCTTCATCCTGGGCCGCCCTCTGTGTT 960
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Qy    961 CCTGTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGTGCCCTGGTGTCTCTATC 1020
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Qy    1021 CTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCATCTTCTTTGCCTTCCTCCAT 1080
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Db    1072 CTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCATCTTCTTTGCCTTCCTCCAT 1131

Qy    1081 TGCTGGCTCAACGCCCTTTGCCGAGATGCTACGATTTGGAGACAGAGATGTTCTACCGGAC 1140
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Qy    1141 TGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAACGTGGTGGTCCATGAC 1200
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Db    1192 TGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAACGTGGTGGTCCATGAC 1251

Qy    1201 TGGCTGTACAGCTGACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGCCCGAGGG 1260
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Db    1252 TGGCTGTACAGCTGACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGCCCGAGGG 1311

Qy    1261 GTAGCCATGCTGGGTGTGTTCCTGGTCTCCCGAGTGGCCCAGTATATCTTCTGCTTC 1320
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Db    1312 GTAGCCATGCTGGGTGTGTTCCTGGTCTCCCGAGTGGCCCAGTATATCTTCTGCTTC 1371

Qy    1321 GTCCTGGGGTTCTTCTATCCCGTCATGCTAACTCTTCCTTGTCATTGGAGGAATGTTG 1380
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Db    1372 GTCCTGGGGTTCTTCTATCCCGTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTG 1431

Qy    1381 AACTTCATGATGCATGACCAGCGCACCGGCCACCGGCCACCGGCCTGCGATCGATGTGGACCATG 1440
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Db    1432 AACTTCATGATGCATGACCAGCGCACCGGCCACCGGCCACCGGCTGCGATGTGATGTGGACCATG 1491

Qy    1441 CTGTTTCTAGGCCAGGGAATCCAGGTCAGCTTGTACTGCCAGGAGTGGTACGCACGGCGG 1500
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Db    1492 CTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGG 1551

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Qy    1561 CATACCTAG 1569
          |||||||||
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